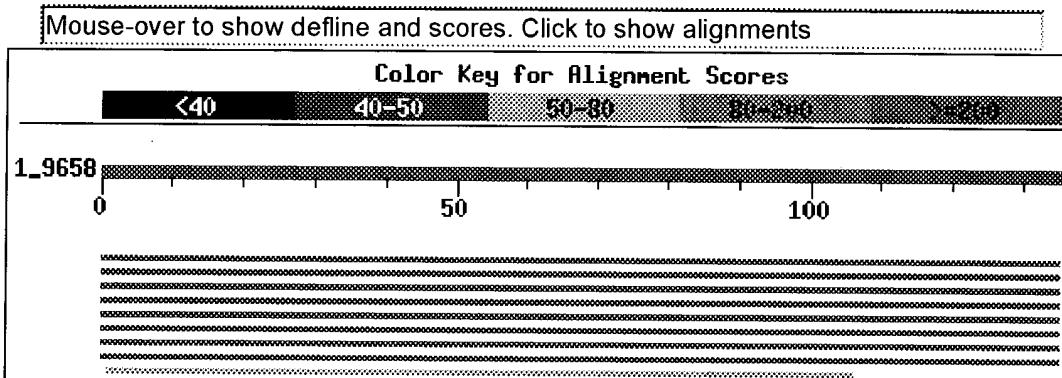
**BLASTP 2.2.6 [Apr-09-2003]**

RID: 1067455426-9658-2307585.BLASTQ3

Query=

(136 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
 1,530,482 sequences; 497,137,717 total letters

Taxonomy reports**Distribution of 355 Blast Hits on the Query Sequence**

| Sequences producing significant alignments: | Score (bits) | E Value |
|---|-----------------|---------|
| gi 284667 pir A43427 neurofilament triplet H1 protein - rat | 334 | 1e-90 |
| gi 71549 pir QFHUH neurofilament triplet H protein - human | 325 | 5e-88 |
| gi 32483416 ref NP_066554.2 neurofilament, heavy polypeptid... | 325 | 5e-88 |
| gi 33302611 sp P12036 NFH_HUMAN Neurofilament triplet H pro... | 322 | 3e-87 |
| gi 27529742 dbj BAA74868.2 KIAA0845 protein [Homo sapiens] | 322 | 3e-87 |
| gi 601931 gb AAA57153.1 neurofilament-H | 317 | 1e-85 |
| gi 284668 pir B43427 neurofilament protein H form H2 (repe... | 313 | 2e-84 |
| gi 24020878 gb AAN40837.1 AF346625_1 heavy neurofilament pr... | 309 | 3e-83 |
| gi 21429606 gb AAM49796.1 heavy neurofilament NF-H [Rattus... | 271 | 8e-72 |
| gi 205686 gb AAA41695.1 heavy neurofilament subunit | 271 | 8e-72 |
| gi 14250426 gb AAH08648.1 AAH08648 Unknown (protein for IMA... | 270 | 1e-71 |
| gi 128127 sp P19246 NFH_MOUSE Neurofilament triplet H prote... | 270 | 2e-71 |
| gi 28972433 dbj EAC65670.1 mKIAA0845 protein [Mus musculus] | 270 | 2e-71 |
| gi 29789026 ref NP_036739.1 neurofilament, heavy polypeptid... | 268 | 8e-71 |
| gi 205680 gb AAA41692.1 high molecular weight neurofilament | 268 | 8e-71 |

| | | | | |
|--------------------------------------|---|-----|-------|--|
| gi 200022 gb AAA39809.1 | neurofilament protein >gi 226537 p... | 267 | 1e-70 | |
| gi 463250 emb CAA83229.1 | Neurofilament protein, high molec... | 267 | 1e-70 | |
| gi 92538 pir S02003 | neurofilament triplet H protein - rat ... | 245 | 6e-64 | |
| gi 462702 sp P16884 NFH_RAT | Neurofilament triplet H protein... | 245 | 6e-64 | |
| gi 37549256 ref XP_291369.3 | similar to KIAA0845 protein [H...] | 207 | 1e-52 | |
| gi 13629976 sp O77788 NFM_BOVIN | Neurofilament triplet M pro... | 152 | 8e-36 | |
| gi 226213 prf 1501343A | neurofilament protein NF-H C term | 147 | 2e-34 | |
| gi 1160355 gb AAB00542.1 | UNC-89 | 136 | 4e-31 | |
| gi 7511618 pir T29757 | protein UNC-89 - Caenorhabditis elegans | 136 | 4e-31 | |
| gi 31746683 gb AAP68958.1 | Uncoordinated protein 89, isoform... | 136 | 4e-31 | |
| gi 25141314 ref NP_491290.2 | UNCoordinated locomotion UNC-8... | 136 | 4e-31 | |
| gi 4885513 ref NP_005373.1 | neurofilament 3 (150kDa medium)... | 113 | 2e-24 | |
| gi 6003540 gb AAF00492.1 AF181990_1 | neurofilament-3 (150 kD... | 111 | 1e-23 | |
| gi 14149397 gb AAK54495.1 AF368231_2 | neurofilament triplet ... | 102 | 9e-21 | |
| gi 423935 pir A46194 | neurofilament protein NF-220, high-mo... | 101 | 1e-20 | |
| gi 18767706 ref NP_571997.1 | neurofilament triplet H1-like ... | 101 | 2e-20 | |
| gi 14549637 gb AAK66966.1 AF255740_1 | histone H1 [Bufo bufo ... | 97 | 2e-19 | |
| gi 23469403 ref ZP_00124737.1 | COG3064: Membrane protein in... | 92 | 1e-17 | |
| gi 32966575 gb AAP92164.1 | histone H1 [Medicago truncatula] | 92 | 1e-17 | |
| gi 13540405 gb AAK29456.1 AF352253_1 | histone H1 [Lens culin... | 91 | 1e-17 | |
| gi 13540403 gb AAK29455.1 AF352252_1 | histone H1 [Lens culin... | 91 | 1e-17 | |
| gi 2981173 gb AAC06245.1 | neurofilament medium subunit [Ser... | 90 | 3e-17 | |
| gi 13540395 gb AAK29451.1 AF352248_1 | histone H1 [Pisum sati... | 90 | 3e-17 | |
| gi 128146 sp P16053 NFM_CHICK | Neurofilament triplet M prote... | 90 | 3e-17 | |
| gi 63686 emb CAA29073.1 | NF-M c-terminus [Gallus gallus] | 90 | 3e-17 | |
| gi 7439660 pir T06257 | histone H1 (clone TH32) - wheat >gi ... | 89 | 8e-17 | |
| gi 21465095 gb AAM54671.1 AF514417_1 | histone H1 [Pisum sati... | 88 | 1e-16 | |
| gi 4106696 dbj BAA36284.1 | ribosome-sedimenting protein [Pi... | 88 | 1e-16 | |
| gi 4996567 dbj BAA78535.1 | ribosome-sedimenting protein [Pi... | 88 | 1e-16 | |
| gi 21465093 gb AAM54670.1 AF514416_1 | histone H1 [Lathyrus a... | 88 | 2e-16 | |
| gi 13540401 gb AAK29454.1 AF352251_1 | histone H1 [Lens culin... | 88 | 2e-16 | |
| gi 13540391 gb AAK29449.1 AF352246_1 | histone H1 [Pisum sati... | 87 | 3e-16 | |
| gi 13540397 gb AAK29452.1 AF352249_1 | histone H1 [Lathyrus s... | 87 | 4e-16 | |
| gi 13540399 gb AAK29453.1 AF352250_1 | histone H1 [Lathyrus s... | 87 | 4e-16 | |
| gi 30420974 gb AAP31307.1 | histone H1 [Lens nigricans] | 87 | 4e-16 | |
| gi 805006 emb CAA56558.1 | pprB [Pseudomonas putida] | 87 | 4e-16 | |
| gi 28867376 ref NP_789995.1 | alginate regulatory protein Al... | 85 | 2e-15 | |
| gi 9630970 ref NP_047640.1 | mucin-like protein [Lymantria d... | 83 | 5e-15 | |
| gi 13540393 gb AAK29450.1 AF352247_1 | histone H1 [Pisum sati... | 83 | 7e-15 | |
| gi 16127671 ref NP_422235.1 | arylesterase-related protein [...] | 82 | 9e-15 | |
| gi 2114317 dbj BAA20035.1 | tegument protein [Equine herpesv... | 82 | 1e-14 | |
| gi 5230788 gb AAD41008.1 AF107026_1 | histone H1 WH1A.3 [Trit... | 81 | 2e-14 | |
| gi 5230790 gb AAD41009.1 AF107027_1 | histone H1 WH1A.4 [Trit... | 81 | 2e-14 | |
| gi 7439656 pir T06241 | histone H1 (clone TH315) - wheat >gi ... | 81 | 2e-14 | |
| gi 30420972 gb AAP31306.1 | histone H1 [Vicia hirsuta] | 80 | 4e-14 | |
| gi 14916992 sp P27806 H1_WHEAT | Histone H1 | 80 | 4e-14 | |
| gi 11558848 emb CAA42529.2 | histone H1 [Triticum aestivum] | 80 | 4e-14 | |
| gi 5230781 gb AAD41005.1 AF107022_1 | histone H1 WH1A.1 [Trit... | 80 | 4e-14 | |
| gi 5230783 gb AAD41006.1 AF107023_1 | histone H1 WH1A.2 [Trit... | 80 | 5e-14 | |
| gi 7428714 pir QFPGM | neurofilament triplet M protein - pig... | 79 | 7e-14 | |
| gi 26986938 ref NP_742363.1 | alginate regulatory protein Al... | 79 | 7e-14 | |
| gi 283442 pir A40215 | TcD antigen - Trypanosoma cruzi | 79 | 1e-13 | |
| gi 161958 gb AAB97874.1 | surface antigen [Trypanosoma cruzi] | 78 | 1e-13 | |
| gi 31213063 ref XP_315475.1 | ENSANGP00000021721 [Anopheles ... | 78 | 2e-13 | |
| gi 28209501 gb AAO37519.1 | histone-like protein [Oryza sati... | 77 | 3e-13 | |
| gi 22963111 ref ZP_00010717.1 | COG3064: Membrane protein in... | 77 | 4e-13 | |
| gi 283024 pir S22322 | histone H1 - wheat | 74 | 3e-12 | |
| gi 2118971 pir I51227 | histone H1A - African clawed frog >g... | 73 | 4e-12 | |

| | | |
|---|----|-------|
| gi 2623960 emb CAA73171.1 histone H1 [Apium graveolens] | 72 | 8e-12 |
| gi 15217879 ref NP_174150.1 prolin-rich protein -related [...] | 72 | 1e-11 |
| gi 30018740 ref NP_830371.1 Internalin protein [Bacillus c...] | 71 | 1e-11 |
| gi 29561775 emb CAD87780.1 SI:dz258D18.1 (novel protein si...) | 71 | 2e-11 |
| gi 15602833 ref NP_245905.1 Tola [Pasteurella multocida] >... | 71 | 2e-11 |
| gi 121955 sp P02254 H1_SALTR Histone H1 >gi 70667 pir HSTR... | 71 | 2e-11 |
| gi 2133786 pir I51116 NF-180 - sea lamprey >gi 632549 gb A... | 71 | 2e-11 |
| gi 121922 sp P06893 H1B_XENLA HISTONE H1B >gi 2118972 pir ... | 70 | 5e-11 |
| gi 70670 pir HSXL1B histone H1B - African clawed frog | 70 | 5e-11 |
| gi 23054984 ref ZP_00081113.1 COG0532: Translation initiat... | 69 | 6e-11 |
| gi 25143299 ref NP_492875.2 pre-mRNA splicing SR protein r... | 69 | 6e-11 |
| gi 9626761 ref NP_041033.1 tegument protein [Equine herpes... | 69 | 8e-11 |
| gi 22538198 ref NP_689049.1 pathogenicity protein, putativ... | 69 | 8e-11 |
| gi 2114319 dbj BAA20036.1 tegument protein [Equine herpesv... | 69 | 8e-11 |
| gi 5230785 gb AAD41007.1 AF107024_1 histone H1 WH1B.1 [Trit... | 68 | 2e-10 |
| gi 121951 sp P06350 H1_ONCMY Histone H1 [Contains: Oncorhyn... | 68 | 2e-10 |
| gi 70668 pir HSTR1R histone H1 - rainbow trout | 68 | 2e-10 |
| gi 121918 sp P06892 H1A_XENLA HISTONE H1A >gi 64775 emb CAA... | 67 | 3e-10 |
| gi 482295 pir A36128 regulatory protein algP - Pseudomonas... | 67 | 3e-10 |
| gi 70669 pir HSXL1A histone H1A - African clawed frog | 67 | 3e-10 |
| gi 15600446 ref NP_253940.1 alginic regulatory protein Al... | 66 | 5e-10 |
| gi 30420970 gb AAP31305.1 histone H1 [Vicia faba] | 66 | 7e-10 |
| gi 4885381 ref NP_005313.1 H1 histone family, member 5 [Ho... | 66 | 7e-10 |
| gi 25012056 ref NP_736451.1 putative peptidoglycan linked ... | 66 | 9e-10 |
| gi 22597168 gb AAN03471.1 unknown protein [Glycine max] | 66 | 9e-10 |
| gi 108359 pir S02571 neurofilament triplet protein H - pig... | 65 | 1e-09 |
| gi 21426893 ref NP_064418.1 histone 1, H1b; histone 1, fam... | 65 | 2e-09 |

Alignments

Get selected sequences Select all Deselect all

>gi|284667|pir||A43427 neurofilament triplet H1 protein - rabbit (fragment)
 gi|601930|gb|AAA57152.1| neurofilament-H
 Length = 606

Score = 334 bits (781), Expect = 1e-90
 Identities = 133/189 (70%), Positives = 134/189 (70%), Gaps = 53/189 (28%)

Query: 1 AKSPAEE-----AKSPAEEAKSP-----AKSPAEEAKSPEKAKSP--- 32
 AKSP E AKSPAEEAKSP AKSPAEEAKSPEKAKSP

Sbjct: 39 AKSPTEGGAAASPEEEAKSPAEEAKSPVKEEAKSPAEEAKSPAEEAKSPEKAKSPVKE 98

Query: 33 -AKSPAEEAKSPVKEEAKSP--AKSPEKAKSPAEEAKSP-----AKSPEK----A 73
 AKSP +AKSPVKEEAKSP AKSPEKAKSPAEEAKSP AKSPEK A

Sbjct: 99 EAKSPEKAKSPVKEEAKSPAEEAKSPEKAKSPAEEAKSPEKAKSPVKEEAKSPEKAKSPAEEA 158

Query: 74 KSPEKAKSP--AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPAEEAKSP--AKSPVKEEA 127
 KSPEKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSPAEEAKSP AKSPVKEEA

Sbjct: 159 KSPEKAKSPAEEAKSPEKAKSPVKEEAKSPEKAKSPAEEAKSPEKAKSPVKEEA 218

Query: 128 KSPEKAKSP 136
 KSPEKAKSP

Sbjct: 219 KSPEKAKSP 227

Score = 326 bits (763), Expect = 2e-88
Identities = 132/194 (68%), Positives = 134/194 (69%), Gaps = 58/194 (29%)

Query: 1 AKSPAEEKSP-----AEAKSPA--KSPAEEKSPEKAKSP---AKSPAEEKSPVKEE 46
AKSPAEEKSP AEAKSPA KSPAEEKSPEKAKSP AKSP +AKSPVKEE
Sbjct: 54 AKSPAEEKSPVKEEAKSPAEEKSPAEEKSPEKAKSPVKEEAKSPEKAKSPVKEE 113

Query: 47 AKSPA--KSPEKAKSPAEAKSP-----AKSPEKAKSP----- 76
AKSPA KSPEKAKSPAEAKSP AKSPEKAKSP
Sbjct: 114 AKSPAEEKSPEKAKSPAEEKSPEKAKSPVKEEAKSPEKAKSPAEEKSPEKAKSPAEAKSP 173

Query: 77 EKAKSP---AKSPEKAKSPVKEEAKSP-----AKSPVKEEAKSPAEEKSP--AKSP 122
EKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSP
Sbjct: 174 EKAKSPVKEEAKSPEKAKSPVKEEAKSPAEEKSPEKAKSPVKEEAKSPEKAKSPAEEKSP 233

Query: 123 VKEEAKSPEKAKSP 136
VKEEAKSPEKAKSP
Sbjct: 234 VKEEAKSPEKAKSP 247

Score = 307 bits (717), Expect = 1e-82
Identities = 134/246 (54%), Positives = 134/246 (54%), Gaps = 110/246 (44%)

Query: 1 AKSPAEEKSPA-----EAKSP-----AKSPAEEKSPEKAKSP----- 32
AKSPAEEKSP EAKSP AKSPAEEKSPEKAKSP
Sbjct: 164 AKSPAEEKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPAEEKSPEKAKSPVKEEAKSPEK 223

Query: 33 AKSPAEEKSPVKEEAKSP-----AKSPEKAKSP-----AEAK 64
AKSPAEEKSPVKEEAKSP AKSPEKAKSP AEAK
Sbjct: 224 AKSPAEEKSPVKEEAKSPEKAKSPKEEAKSPAEEKSPEKAKSPEKAKSPVKEEVKSPAEEK 283

Query: 65 SP-----AKSPEKAKSP-----EKAKSP---AKSPEK 88
SP AKSPEKAKSP EKAKSP AKSPEK
Sbjct: 284 SPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 343

Query: 89 AKSPVKEEAKSP--AKSPVKEEAKSP-----EAKSP--AKSPVKEEAKSP 130
AKSPVKEEAKSP AKSPVKEEAKSP EAKSP AKSPVKEEAKSP
Sbjct: 344 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 403

Query: 131 EKAKSP 136
EKAKSP
Sbjct: 404 EKAKSP 409

Score = 240 bits (559), Expect = 2e-62
Identities = 117/238 (49%), Positives = 120/238 (50%), Gaps = 104/238 (43%)

Query: 1 AKSPAEEKSPAEEKSP--AKSPA--EAKSPEKAKSP---AKSPAEEKSPVKEEAKSP-- 50
AKSP E KSPAEEKSP AKSP EAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 270 AKSPVEVKSPAEEKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 329

Query: 51 -----AKSPEKAKSPA--EAKSP-----AKSPEKAKSPEKAKSP----- 82
AKSPEKAKSP EAKSP AKSPEKAKSPEKAKSP
Sbjct: 330 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSP 389

Query: 83 -----AKSPEKAKSPVKEEAKSPAK-SPVKEEAK----- 110

AKSPEKAKSPVKEEKSP K +P KEE K
 Sbjct: 390 EKAKSPVKEEKSPPEKAKSPVKEEKSPPEKETPKKEEVKVKEPPKKVEETAPAPPKVEKD 449

Query: 111 -----SPAEEK-----SPAEEKSPVKEEKSPPEK---AK 134
 S AEEK +PAK KEEK EK AK
 Sbjct: 450 SKKDEAPKKEAPKPAVEKPKESTAEAKKDEAKKKAAAPAKMEGKEEKPKAKEVAK 507

Score = 212 bits (493), Expect = 6e-54
 Identities = 86/119 (72%), Positives = 89/119 (74%), Gaps = 27/119 (22%)

Query: 45 EEAKSP----AKSP-EKAKSPAEAKSP----AKSPEKAKSP--AKSPEKAKSPV 93
 EEAKSP A SP E+AKSPAEAKSP AKSP +AKSP +AKSP AKSPEKAKSPV
 Sbjct: 37 EEAKSPTEGGAASPEEEAKSPAEAKSPVKEEKSPAEAKSPAEAKSPAEAKSPVKEEKSPV 96

Query: 94 KEEAKSP--AKSPVKEEKSPAEAKSP-----AKSPVKEEKSPPEKAKSP 136
 KEEKSP AKSPVKEEKSPAEAKSP AKSPVKEEKSPPEKAKSP
 Sbjct: 97 KEEAKSPPEKAKSPVKEEKSPAEAKSPPEKAKSPVKEEKSPPEKAKSPVKEEKSP 155

Score = 142 bits (328), Expect = 7e-33
 Identities = 97/233 (41%), Positives = 109/233 (46%), Gaps = 106/233 (45%)

Query: 1 AKSPA--EAKSPAEAKSP--AKSPA--EAKSPPEKAKSP----AKSPAEAKSPVKEEKSP 50
 AKSP EAKSP +AKSP AKSP EAKSPPEKAKSP AKSP +AKSPVKEEKSP
 Sbjct: 358 AKSPVKEEKSPPEKAKSPVKEEKSPPEKAKSPVKEEKSPPEKAKSPVKEEKSP 417

Query: 51 AK-----SP----EKA-K-SPAEEK- 64
 K +P EK K S AEAK
 Sbjct: 418 EKETPKKEEVKVKEPPKKVEETAPAPPKVEKDSKKDEAPKKEAPKPAVEKPKESTAEAKK 477

Query: 65 -----SPA-----SP-EKA---KSPE--KAKSPAKS---PEKAKSPVKEEA 97
 +PAK P EK K PE KAK P+K PEK K KEE
 Sbjct: 478 DEAEDKKAAAPAKMEGKEEKPKAKEVAKKEPEDAKAKEPSKPKTEKEPEKPK---KEE- 533

Query: 98 KSPAKSPV---KEEKSPAE-AKSPAKSPVKEEKSP---P----EKA-KS 135
 +PA +PV KEEA+ P E K+ AK+ KE+ K+ P EKA KS
 Sbjct: 534 -TPA-APVKKEAKEEARKPEEKPKTEAKA--KEDDKALSKEPSKPKTEKAES 582

[>gi|71549|pir||QFHUH neurofilament triplet H protein - human
 gi|1841430|emb|CAA33366.1| [>] heavy neurofilament subunit [Homo sapiens]
 Length = 1020

Score = 325 bits (760), Expect = 5e-88
 Identities = 130/182 (71%), Positives = 132/182 (72%), Gaps = 46/182 (25%)

Query: 1 AKSPAEAKSPAEAKSPAK----SPAEEKSPPEKAKSP---AKSPAEAKSPVKEEKSP- 51
 AKSPAE KSP +AKSPAK SPAEEKSPPEKAKSP AKSPAEAKSPVKEEKSP
 Sbjct: 572 AKSPAEVKSPPEKAKSPAEAKSPAEAKSPPEKAKSPVKEEKSPAEAKSPVKEEKSP 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKA-KSP---AKSP 86
 KSPEKAKSP EAKSP AKSPEKAKSP EKA-KSP AKSP
 Sbjct: 632 VKSPEKAKSPTEAKSPEKAKSPKEEAKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSP 691

Query: 87 EKAKSPVKEEKSP--AKSPVKEEKSPAEAKSP-----AKSPVKEEKSPPEKAK 134

EKAKSPVKEEKAKSP AKSPVKEEKAKSP +AKSP AKSPVKEEKAKSPEKAK
Sbjct: 692 EKAKSPVKEEKAKSPEKAKSPVKEEKAKSPEKAKSPVKEEKAKTPEKAKSPVKEEKAKSPEKAK 751

Query: 135 SP 136
SP
Sbjct: 752 SP 753

Score = 316 bits (738), Expect = 3e-85
Identities = 131/202 (64%), Positives = 132/202 (65%), Gaps = 66/202 (32%)

Query: 1 AKSPAE-----AKS P AEAKS P-----AKS PAE 22
AKSPAE AKSP EAKSP AKS PAE
Sbjct: 538 AKSPAEVKSP EAKS PAAKEEAKS PPEAKS PEAKEEAKS PAEVKSP EAKS PAAKEEAKS PAE 597

Query: 23 AKSPEKAKSP---AKSPAEEKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPAEEKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 598 AKSPEKAKSPVKEEAKSPAEEKSPVKEEAKSPAEVKSPEKAKSPTEKEEAKSPEKAKSPEK 657

Query: 73 --AKSPEKAKSP---AKSPEKAKSPVKEAKSP--AKSPVKEAKSP-----AEAK 116
AKSPEKAKSP AKSPEKAKSPVKEAKSP AKSPVKEAKSP EAK
Sbjct: 658 EEAKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAK 717

Query: 117 SP-AKSPVKEEAKSPEAKSP 136
 SP AKSPVKEEAK+PEAKSP
Sbjct: 718 SPEAKSPVKEEAKTPEAKSP 739

Score = 309 bits (723), Expect = 3e-83
Identities = 130/196 (66%), Positives = 130/196 (66%), Gaps = 60/196 (30%)

Query: 1 AKSPA--EAKSPAEAKSP---AKSPAEEKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP EAKSPAEAKSP AKSPAEEAKSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 516 AKSPVKEEAKSPAEAKSPEKEEAKSPAEVKSPAEKSPAKEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA----- KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 576 AEVKSPEKAKSPAKEEAKSPAEEAKSPEKAKSPVKEEAKSPAEEAKSPVKEEAKSPAEVKSP 635

Query: 77 EKAKSP---AKSPEAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAKSP--AK 120
 EKAKSP AKSPEAKSP KEEAKSP AKSPVK EAKSP AEAKSP AK
 Sbjct: 636 EKA
KSPTKEEAKSPEAKSPEKEEAKSPEAKSPVKA
EAKSPEAKSPVKA
EAKSPEKAK 695

Query: 121 SPVKKEAKSPEKAKSP 136
 SPVKKEAKSPEKAKSP
Sbjct: 696 SPVKKEAKSPEKAKSP 711

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPAKSPA-EKSPEK-AKSP---AKS PEA KSPEAKSPVKEEAKSPA--KSPEAKSP A 61
E KSP PAE A SPEK AKSP AKS PEA KSPEAKSP VKEEAKSPA KSPEAKSP
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSP EAKSPVKEEAKSPA EVKSPEAKSPAKE 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEAKSP- 100
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEAKSP

Sbjct: 557 EAKSPPEAKSPEKEEAKSPAEVKSPEKAKSPAEEAKSPAEEKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPAEEKSP--AKSPVKEEAKSPEKAKSP 136
AKSPVKEEAKSPA KSP AKSP KEEAKSPEKAKSP

Sbjct: 617 EAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSP 65.5

Score = 261 bits (608), Expect = 1e-68

Identities = 121/235 (51%), Positives = 124/235 (52%), Gaps = 99/235 (42%)

Query: 1 AKSPA--EAKSPAEEKSP---AKSPAEEKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP EAKSPAEEKSP AKSPA EAKSPEKAKSP AKSP +AKSP KEEAKSP

Sbjct: 604 AKSPVKEEAKSPAEEKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSP 663

Query: 51 -----AKSPEKAKSP--AEAKSP-----AKSPEKAKSP-----EKAK 80
AKSPEKAKSP AEAKSP AKSPEKAKSP EKAK

Sbjct: 664 EKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAK 723

Query: 81 SP----AKSPEKAKSPVKEEAKSP----- 100
SP AK+PEKAKSPVKEEAKSP

Sbjct: 724 SPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPADKFPE 783

Query: 101 -AKSPVKEEAKSPAEEKSP-----AKSPVKEEAKSPE-KAKSP 136
AKSPVKEE KSP +AKSP KSPVKEE K E K K P

Sbjct: 784 KAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEVKSPVKEEKPQEVKVKEP 838

Score = 210 bits (488), Expect = 3e-53

Identities = 117/272 (43%), Positives = 124/272 (45%), Gaps = 139/272 (51%)

Query: 1 AKSPAEEKSP--AEAKSP--AKSP--AEAKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP

Sbjct: 660 AKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 719

Query: 51 -----AKSPEKAKSP--EAKSP--AKSPEKAK-----SPEKAKSPAK---SP- 86
AK+PEKAKSP EAKSP AKSPEKAK SPE AK+PAK SP

Sbjct: 720 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPE-AKTPAKEEARSPA 778

Query: 87 -----EAKSPVKEE-----AKSP-----AKSPVKE----- 107
EAKSPVKEE AKSP KSPVKE

Sbjct: 779 DKFPEKAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEVKSPVKEEKPQEVKVKEP 838

Query: 108 -----EAKSPA-----EAK----- 116
E K+PA EAK

Sbjct: 839 PKKAEEEKAPATPKTEEKDKSKKEEAPKKEAPKPKVEEKKEPAVEKPESKVEAKKEEAE 898

Query: 117 -----SPEAKSPVKEEAKSPEK---AK 134
+PAK VKE+AK EK AK

Sbjct: 899 DKKKVPTPEKEAPAKVEVKEDAKPKEKTEVAK 930

Score = 100 bits (229), Expect = 3e-20

Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPAAEKSPA--EAKSPA-----KSPA--EAKSPEKAKSP---AKSPA-----EA 39
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E

Sbjct: 762 KSP-EAKTPAKEEARSPADKFPEKAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEV 820

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
 KSPVKE E K+PA K+ EK A K P
 Sbjct: 821 KSPVKEEKPKQEVKVKEPPKAAEEEKAPATPKTEEKDSKKEEAPKKEAPKPKVEEKKEP 880

Query: 61 A-----EAK-----SPA-----SP-EKA---KSPE--KAKS 81
 A EAK +PAK P EK K P+ KAK
 Sbjct: 881 AVEKPKEVKVEAKKEEAEDKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 940

Query: 82 PAKSPEKAKSPVKEAKSPAKSPVKEE-AKSPA-E-AKSPA-KSPVKEEAKS----P---- 130
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
 Sbjct: 941 PSKPAEK----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 991

Query: 131 EKA-KS 135
 EKA KS
 Sbjct: 992 EKAEKS 997

Score = 97.8 bits (223), Expect = 2e-19
 Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA-EAKSP---AKSPVKEEAKSPEKAKSP 136
 E+ KSP EEA SP AKSPVKEEAKSPA-EAKSP AKSP E KSPEKAKSP
 Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPA-EAKSPEKEEAKSP--AEVKSPEKAKSP 553

[>gi|32483416|ref|NP_066554.2|] neurofilament, heavy polypeptide 200kDa; Neurofilament, heavy polypeptide; neurofilament, heavy polypeptide (200kD)
 [Homo sapiens]
 Length = 1020

Score = 325 bits (760), Expect = 5e-88
 Identities = 130/182 (71%), Positives = 132/182 (72%), Gaps = 46/182 (25%)

Query: 1 AKSPA-EAKSPA-EAKSPAK---SPA-EAKSPEKAKSP---AKSPA-EAKSPVKEEAKSPA- 51
 AKSPA EAKSP +AKSPA SPA-EAKSPEKAKSP AKSPA-EAKSPVKEEAKSPA
 Sbjct: 572 AKSPA-EVKSP-EAKSPA-EAKSPEKEAKSPVKEEAKSPA-EAKSPVKEEAKSPA 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EAKSP---AKSP 86
 KSPEKAKSP EAKSP AKSPEKAKSP EAKSP AKSP
 Sbjct: 632 VKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSPEKAKSPVKA-EAKSPEKAKSPVKA-EAKSP 691

Query: 87 EKAKSPVKEEAKSP--AKSPVKEEAKSPA-EAKSP-----AKSPVKEEAKSPEKAK 134
 EKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAK
 Sbjct: 692 EKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAK 751

Query: 135 SP 136
 SP
 Sbjct: 752 SP 753

Score = 316 bits (738), Expect = 3e-85
 Identities = 131/202 (64%), Positives = 132/202 (65%), Gaps = 66/202 (32%)

Query: 1 AKSPA-E-----AKSPA-EAKSP-----AKSPA-E 22
 AKSPA E AKSP EAKSP AKSPA
 Sbjct: 538 AKSPA-EVKSP-EAKSPA-EAKSPEAKSPEKEEAKSPA-EVKSP-EAKSPA 597

Query: 23 AKSPEKAKSP---AKSPAEEKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPAEEKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 598 AKSPEKAKSPVKEEAKSPAEEKSPVKEEAKSPAEVKSPEKAKSPTEAKSPEKAKSPEK 657

Query: 73 --AKSPEKAKSP---AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
AKSPEKAKSP AKSPEKAKSPVKA EAKSP AKSPVKEEAKSP EAK
Sbjct: 658 EEAKSPEKAKSPVKAEEKSPEKAKSPVKAEEKSPEKAKSPVKEEAKSPEKAKSPVKEEAK 717

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAK+PEKAKSP
Sbjct: 718 SPEKAKSPVKEEAKTPEKAKSP 739

Score = 309 bits (723), Expect = 3e-83
Identities = 130/196 (66%), Positives = 130/196 (66%), Gaps = 60/196 (30%)

Query: 1 AKSPA--EAKSPAEEKSP---AKSPAEEKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP EAKSPAEEKSP AKSPAEEKSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 516 AKSPVKEEAKSPAEEKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 576 AEVKSPEKAKSPAEEKSPEAKSPEKAKSPVKEEAKSPAEEKSPVKEEAKSPAEVKSP 635

Query: 77 EKAKSP---AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAKSP--AK 120
EKAKSP AKSPEKAKSP KEEAKSP AKSPVKA EAKSP AEAKSP AK
Sbjct: 636 EKAKSPTEAKSPEKAKSPEKEEAKSPEKAKSPVKAEEKSPEKAKSPVKAEEKSPEKAK 695

Query: 121 SPVKEEAKSPEKAKSP 136
SPVKEEAKSPEKAKSP
Sbjct: 696 SPVKEEAKSPEKAKSP 711

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPAKSPA-EKSPEK-AKSP---AKSPAEEKSPVKEEAKSPA--KSPEKAKSPA-- 61
E KSP PAE A SPEK AKSP AKSPAEEKSP KEEAKSPA KSPEKAKSPA
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPAEEKSPEKEEAKSPAEVKSPEKAKSPA 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP- 100
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP
Sbjct: 557 EAKSPPEAKSPEKEEAKSPAEVKSPEKAKSPAEEKSPEAKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPAEEKSP--AKSPVKEEAKSPEKAKSP 136
AKSPVKEEAKSPAEE KSP AKSP KEEAKSPEKAKSP
Sbjct: 617 EAKSPVKEEAKSPAEVKSPEKAKSPTEAKSPEKAKSP 655

Score = 228 bits (531), Expect = 8e-59
Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPAEEKSP--AEAKSP--AKSP--AEAKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 660 AKSPEKAKSPVKAEEKSPEKAKSPVKAEEKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 719

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75
 AK+PEKAKSP EAKSP AKSPEKAK+
 Sbjct: 720 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKTLDVKSPEAKTPAKEEARSPAD 779

Query: 76 --PEKAKSPA-----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPAEEAKSPA 120
 PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K
 Sbjct: 780 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPEAKSPLKEDAKAPEKEIPKKEEV 834

Query: 121 SPVKEEAKSPEKAKSP 136
 VKE K E+ K+P
 Sbjct: 835 --VKEPPKAEEEKAP 848

Score = 100 bits (229), Expect = 3e-20
 Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPAEAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP---AKSPA-----EA 39
 KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E
 Sbjct: 762 KSP-EAKTPAKEEARSPADKFPEKAKSPVKEEVKSPEAKSPLKEDAKAPEKEIPKKEEV 820

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
 KSPVKE E K+PA K+ EK A K P
 Sbjct: 821 KSPVKEEEKPQEVKVKEPPKAAEEKAPATPKTEEKDSKKEEAPKKEAPKPKVEEKKEP 880

Query: 61 A-----EAK-----SPA-----SP-EKA---KSPE--KAKS 81
 A EAK +PAK P EK K P+ KAK
 Sbjct: 881 AVEKPKESKVEAKKEEAEDKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEAPDAAKE 940

Query: 82 PAKSPEKAKSPVKEEAKSPAksPVKEE-AKSPA-EAKSPAksPVKEEAKS-----P----- 130
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
 Sbjct: 941 PSKPAEK----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 991

Query: 131 EKA-KS 135
 EKA KS
 Sbjct: 992 EKAEKS 997

Score = 97.8 bits (223), Expect = 2e-19
 Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPAEEAKSP---AKSPVKEEAKSPEKAKSP 136
 E+ KSP EEA SP AKSPVKEEAKSPAEEAKSP AKSP E KSPEKAKSP
 Sbjct: 499 EETKSPPAAAASPEKEAKSPVKEEAKSPAEEAKSPEKEAKSP--AEVKSPEKAKSP 553

[>gi|33302611|sp|P12036|NFH_HUMAN [>gi|6470331|gb|AAF13722.1|AF203032_1] Neurofilament triplet H protein (200 kDa neur (Neurofilament heavy polypeptide) (NF-H)
 Length = 1026

Score = 322 bits (754), Expect = 3e-87
 Identities = 130/188 (69%), Positives = 132/188 (70%), Gaps = 52/188 (27%)

Query: 1 AKSPAEEAKSPAEEAKSPA-----SPAEEAKSPEKAKSP---AKSPAEEAKSPVKEEAKSPA- 51
 AKSPAEE KSP +AKSPA SPAEEAKSPEKAKSP AKSPAEEAKSPVKEEAKSPA
 Sbjct: 572 AKSPAEEVKSPPEAKSPAEEAKSPAEEAKSPEKAKSPVKEEAKSPAEEAKSPVKEEAKSPA 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKAKSP-- 82
KSPEKAKSP EAKSP AKSPEKAKSP EKAKSP
Sbjct: 632 VKSPEKAKSPVKEEAKSPEKAKSPEKEEAKSPEKAKSPVKAEEKSPEKAKSPVK 691

Query: 83 --AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPAEEKSP-----AKSPVKEEAK 128
AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAK
Sbjct: 692 AEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAK 751

Query: 129 SPEKAKSP 136
SPEKAKSP
Sbjct: 752 SPEKAKSP 759

Score = 313 bits (732), Expect = 2e-84
Identities = 131/208 (62%), Positives = 132/208 (63%), Gaps = 72/208 (34%)

Query: 1 AKSPA-----AKSPAEEKSP-----AKSPA 22
AKSPA AKSP EAKSP AKSPA
Sbjct: 538 AKSPAEVKSPEKAKSPAEEAKSPPEAKSPEKEEAKSPAEVKSPEKAKSPAEEAKSPA 597

Query: 23 AKSPEKAKSP---AKSPAEEKSPVKEEAKSPA--KSPEKAKSP--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPAEEKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 598 AKSPEKAKSPVKEEAKSPAEEAKSPVKEEAKSPAEVKSPEKAKSPVKEEAKSPEKAKSP 657

Query: 73 AKSPEK--AKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP----- 112
AKSPEK AKSP AKSPEKAKSPVKEEAKSPVKAEEKSPEKAKSPVKAEEKSPEKAKSPVKEEAKSPEKAKSP 717

Query: 113 --AEAKSP--AKSPVKEEAKSPEKAKSP 136
EAKSP AKSPVKEEAK+PEKAKSP
Sbjct: 718 VKEEAKSPEKAKSPVKEEAKTPEKAKSP 745

Score = 307 bits (717), Expect = 1e-82
Identities = 130/202 (64%), Positives = 130/202 (64%), Gaps = 66/202 (32%)

Query: 1 AKSPA--EAKSPAEEKSP---AKSPAEEKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP EAKSPAEEKSP AKSPA KSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 516 AKSPVKEEAKSPAEEAKSPEKEEAKSPAEVKSPEKAKSPAEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 576 AEVKSPEKAKSPAEEAKSPAEEAKSPEKAKSPVKEEAKSPAEEAKSPVKEEAKSPAEVKSP 635

Query: 77 EKAKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
EKAKSP AKSPEKAKSP KEEAKSP AKSPVKEEAKSP EAKSP AEAK
Sbjct: 636 EKAKSPVKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKAEEKSPEKAKSPVKAEEK 695

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAKSPEKAKSP
Sbjct: 696 SPEKAKSPVKEEAKSPEKAKSP 717

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPAKSPA-EKSPEK-AKSP---AKSPEAEKSPVKEEAKSPA--KSPEAKSPA-- 61
 E KSP PAE A SPEK AKSP AKSPEAKSP KEEAKSPA KSPEAKSPA
 Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA-EAKSPEKEEAKSPA-EAKSPVKEEAKSPA 556

Query: 62 EAKSP--AKSPEK-----AKSPEAKSP-----AKSPEAKSPVKEEAKSP- 100
 EAKSP AKSPEK KSPEAKSP AKSPEAKSPVKEEAKSP
 Sbjct: 557 EAKSPPEAKSPEKEEAKSPA-EVKSP-EAKSPEAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPA-EAKSP--AKSPVKEEAKSPEAKSP 136
 AKSPVKEEAKSPA KSP AKSP KEEAKSPEAKSP
 Sbjct: 617 EAKSPVKEEAKSPA-EVKSP-EAKSPEAKSPVKEEAKSP 655

Score = 228 bits (531), Expect = 8e-59
 Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPEAEKSP--AEAKSP--AKSP--AEAKSPEAKSP---AKSPEAEKSPVKEEAKSP 50
 AKSP +AKSP AEAKSP AKSP AEAKSPEAKSP AKSP +AKSPVKEEAKSP
 Sbjct: 666 AKSPEAKSPVKA-EAKSPEAKSPVKA-EAKSPEAKSPVKEEAKSPEAKSPVKEEAKSP 725

Query: 51 -----AKSPEAKSPA--EAKSP--AKSPEAKS----- 75
 AK+PEAKSP EAKSP AKSPEAK+
 Sbjct: 726 EAKSPVKEEAKTP-EAKSPVKEEAKSPEAKSPEAKTL-DVKSPEAKTP-AKEEARS-PAD 785

Query: 76 --PEKAKSPA---SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA-EAKSPAK 120
 PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K
 Sbjct: 786 KFPEKAKSPVKEEVKSPEAKSPLKEDAKAPEKEIPKKEEVKSPVKEEK-PQEVK--- 840

Query: 121 SPVKEEAKSPEAKSP 136
 VKE K E+ K+P
 Sbjct: 841 --VKEPPKAAEEEKAP 854

Score = 100 bits (229), Expect = 3e-20
 Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPAEAKSPA--EAKSPA-----KSPA--EAKSPEAKSP---AKSPA-----EA 39
 KSP EAK+PA EA+SPA KSP E KSPEAKSP AK+P E
 Sbjct: 768 KSP-EAKTP-AKEEARS-PADKFPEAKSPVKEEVKSPEAKSPLKEDAKAPEKEIPKKEEV 826

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
 KSPVKE E K+PA K+ EK A K P
 Sbjct: 827 KSPVKEEKPKQEVKVKEPPKAAEEEKAPATPKTEEKDKSEEAPKKEAPKPKVEEKKEP 886

Query: 61 A-----EAK-----SPA-----SP-EKA---KSPE--KAKS 81
 A EAK +PAK P EK K P+ KAK
 Sbjct: 887 AVEKP-KESKVEAKKEAEDKKKVPTPEKEAPAKVEVKEAPKKEAPKPKVEEKKEP 946

Query: 82 PAKSPEAKSPVKEEAKSPA-KSPVKEE-AKSPA-EAKSPA-KSPVKEEAKS----P---- 130
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
 Sbjct: 947 PSKPAEK----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 997

Query: 131 EKA-KS 135
 EKA KS
 Sbjct: 998 EKA-EKS 1003

Score = 97.8 bits (223), Expect = 2e-19
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EAKAKSPVKEEAKSP---AKSPVKEEAKSPAEEKSP---AKSPVKEEAKSPEKAKSP 136
E+ KSP EEA SP AKSPVKEEAKSPAEEKSP AKSP E KSPEKAKSP
Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPAEEKSPEKEEAKSP--AEVKSPEKAKSP 553

[>] >gi|27529742|dbj|BAA74868.2| [>] KIAA0845 protein [Homo sapiens]
Length = 1034

Score = 322 bits (754), Expect = 3e-87
Identities = 130/188 (69%), Positives = 132/188 (70%), Gaps = 52/188 (27%)

Query: 1 AKSPAEEKSPAEAKSPAK---SPAEEKSPEKAKSP---AKSPAEEKSPVKEEAKSPA- 51
AKSPAEE KSP +AKSPAK SPAEEKSPEKAKSP AKSPAEEKSPVKEEAKSPA
Sbjct: 580 AKSPAEVKSPPEKAKSPAKEEAKSPAEEKSPEKAKSPVKEEAKSPAEEKSPVKEEAKSPA 639

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKAKSP-- 82
KSPEKAKSP EAKSP AKSPEKAKSP EKAKSP
Sbjct: 640 VKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKAEEKSPEKAKSPVKA 699

Query: 83 --AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPAEEKSP-----AKSPVKEEAK 128
AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAK
Sbjct: 700 AEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAK 759

Query: 129 SPEKAKSP 136
SPEKAKSP
Sbjct: 760 SPEKAKSP 767

Score = 313 bits (732), Expect = 2e-84
Identities = 131/208 (62%), Positives = 132/208 (63%), Gaps = 72/208 (34%)

Query: 1 AKSPAEE-----AKSPAEEKSP-----AKSPAEE 22
AKSPAEE AKSP EAKSP AKSPAEE
Sbjct: 546 AKSPAEVKSPPEKAKSPAKEEAKSPPEAKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSPA 605

Query: 23 AKSPEKAKSP---AKSPAEEKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPAEEKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 606 AKSPEKAKSPVKEEAKSPAEAKSPVKEEAKSPAEVKSPPEKAKSPVKEEAKSPEKAKSP 665

Query: 73 AKSPEK--AKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP----- 112
AKSPEK AKSP AKSPEKAKSPVKA EAKSP AKSPVKEEAKSP
Sbjct: 666 AKSPEKEEAKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSP 725

Query: 113 --AEAKSP--AKSPVKEEAKSPEKAKSP 136
EAKSP AKSPVKEEAK+PEKAKSP
Sbjct: 726 VKEEAKSPEKAKSPVKEEAKTPEKAKSP 753

Score = 307 bits (717), Expect = 1e-82
Identities = 130/202 (64%), Positives = 130/202 (64%), Gaps = 66/202 (32%)

Query: 1 AKSPA--EAKSPAEEKSP---AKSPAEEKSPEKAKSP---AKSPAEEKSPVKEEAKSP 50
AKSP EAKSPAEEKSP AKSPAEE KSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 524 AKSPVKEEAKSPEAKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSPPEAKSPEKEEAKSP 583

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 584 AEVKSPEKAKSPAEEAKSPAEEAKSPEKAKSPVKEEAKSPAEEAKSPVKEEAKSPAEVKSP 643

Query: 77 EAKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
EAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAK
Sbjct: 644 EKAKSPTKEEAKSPEKAKSPEKAKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAK 703

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAKSPEKAKSP
Sbjct: 704 SPEKAKSPVKEEAKSPEKAKSP 725

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPAKSPA-EKSPEK-AKSP---AKSPAEEAKSPVKEEAKSPA--KSPEKAKSPA-- 61
E KSP PAE A SPEK AKSP AKSPAEEAKSP KEEAKSPA KSPEKAKSPA
Sbjct: 508 ETKSP---PAEEAASPEKEAKSPVKEEAKSPAEEAKSPEKEEAKSPAEVKSPEKAKSPA 564

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP- 100
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP
Sbjct: 565 EAKSPPPEAKSPEKEEAKSPAEVKSPEKAKSPAEEAKSPAEEAKSPEKAKSPVKEEAKSPA 624

Query: 101 -AKSPVKEEAKSPAEEAKSP--AKSPVKEEAKSPEKAKSP 136
AKSPVKEEAKSPA KSP AKSP KEEAKSPEKAKSP
Sbjct: 625 EAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSP 663

Score = 228 bits (531), Expect = 8e-59
Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPAEEAKSP--AEAKSP--AKSP--AEAKSPEKAKSP---AKSPAEEAKSPVKEEAKSP 50
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 674 AKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 733

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75
AK+PEKAKSP EAKSP AKSPEKAK+
Sbjct: 734 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPAD 793

Query: 76 --PEKAKSPAK---SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPAEEAKSPAK 120
PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K
Sbjct: 794 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPEVKEEEEK-PQEVK--- 848

Query: 121 SPVKEEAKSPEKAKSP 136
VKE K E+ K+P
Sbjct: 849 --VKEPPKAAEEEKAP 862

Score = 100 bits (229), Expect = 3e-20
Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPAEEAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP---AKSPA-----EA 39
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E
Sbjct: 776 KSP-EAKTPAKEEARSPADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 834

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
 KSPVKE E K+PA K+ EK A K P
 Sbjct: 835 KSPVKEEEKPQEVKVEPPKAAEEEKAPATPKTEEKDSKKEAPKKEAPKPKVEEKKEP 894

Query: 61 A-----EAK-----SPAK-----SP-EKA---KSPE--KAKS 81
 A EAK +PAK P EK K P+ KAK
 Sbjct: 895 AVEKPKESKVEAKKEEAEDKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 954

Query: 82 PAKSPEKAKSPVKEEAKSPAKSPVKEE-AKSPA-EAKSPA-KSPEKAKSP---P---- 130
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
 Sbjct: 955 PSKPAEK----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 1005

Query: 131 EKA-KS 135
 EKA KS
 Sbjct: 1006 EKAEKS 1011

Score = 97.8 bits (223), Expect = 2e-19
 Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA-EAKSP---AKSPVKEEAKSPEKAKSP 136
 E+ KSP EEA SP AKSPVKEEAKSPA-EAKSP AKSP E KSPEKAKSP
 Sbjct: 507 EETKSPPAEEASPEKEAKSPVKEEAKSPA-EAKSPEKEEAKSP--AEVKSPEKAKSP 561

[>] >gi|601931|qb|AAA57153.1| neurofilament-H
 Length = 511

Score = 317 bits (741), Expect = 1e-85
 Identities = 127/172 (73%), Positives = 130/172 (75%), Gaps = 36/172 (20%)

Query: 1 AKSPA--EAKSPA-EAKSPA--KSPAEAKSPEKAKSP---AKSPAEAKSPVKEEAKSP-- 50
 AKSP EAKSP +AKSP KSPAEAKSPEKAKSP AKSP +AKSPVKEEAKSP
 Sbjct: 194 AKSPEKEEAKSPEKAKSPVKEEVKSPAEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 253

Query: 51 AKSPEKAKSPA--EAKSP-----AKSPEKAKSPEKAKSP---AKSPEKAKSPV 94
 AKSPEKAKSP EAKSP AKSPEKAKSPEKAKSP AKSPEKAKSPV
 Sbjct: 254 AKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPV 313

Query: 95 EEAKSP-----AKSPVKEEAKSPA-EAKSP--AKSPVKEEAKSPEKAKSP 136
 EEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAKSP
 Sbjct: 314 EEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSP 365

Score = 312 bits (729), Expect = 4e-84
 Identities = 132/219 (60%), Positives = 132/219 (60%), Gaps = 84/219 (38%)

Query: 2 KSPAEAKSPA-EAKSP--AKSPAEAKSPEKAKSPA-----SPA 37
 KSPAEAKSPA-EAKSP AKSPAEAKSPEKAKSP K SPA
 Sbjct: 93 KSPAEAKSPA-EAKSPEKAKSPAEAKSPEKAKSPVKEEAKSPEKAKSPVVEVKSPA 152

Query: 38 EAKSP-----VKEEAKSPA--KSPEKAKSPA--EAKSP-----AKSPEKAKSP- 76
 EAKSP VKEEAKSPA KSPEKAKSP EAKSP AKSPEKAKSP
 Sbjct: 153 EAKSPEKAKSPVKEEAKSPA-EAKSPEKAKSPEKEEAKSPEKAKSPVKEEAKSPEKAKSPV 212

Query: 77 -----EAKSP---AKSPEKAKSPVKEEAKSP-----AKSPVKEEAKSP- 112
 EAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP